GENETICS

A PERIODICAL RECORD OF INVESTIGATIONS
BEARING ON HEREDITY AND VARIATION

FOUNDED IN 1916

and published by

THE GENETICS SOCIETY OF AMERICA

VOLUME 164, MAY–AUGUST 2003

EDITORIAL BOARD

Elizabeth W. Jones, *Editor-in-Chief*
Carnegie Mellon University, Pittsburgh, PA

Montserrat Aguadé (2005)
Universitat de Barcelona

Kathryn V. Anderson (2005)
Sloan-Kettering Institute

Philip Anderson (2005)
University of Wisconsin

Brenda J. Andrews (2003)
University of Toronto

Norman Arnheim (2005)
University of Southern California

Marjorie A. Asmussen (2003)
University of Georgia

Bonnie Bartel (2005)
Rice University

Bonnie L. Bassler (2004)
Princeton University

David Begun (2005)
University of California, Davis

Joy Bergelson (2005)
University of Chicago

James A. Birchler (2005)
University of Missouri

David Botstein (2003)
Stanford University School of Medicine

Anthony H. D. Brown (2003)
CSIRO Division of Plant Industry

Vicki L. Chandler (2004)
University of Arizona

Deborah Charlesworth (2005)
University of Edinburgh

Gary A. Churchill (2003)
The Jackson Laboratory

Rebecca Doerge (2005)
Purdue University

Thomas A. Eickbush (2005)
University of Rochester

Laurent Excoffier (2005)
University of Bern

Marcus W. Feldman (2003)
Stanford University

Yun-Xin Fu (2004)
University of Texas, Houston

Kent Golic (2005)
University of Utah

David Jonah Grunwald (2004)
University of Utah

Chris Haley (2003)
Roslin Institute (Edinburgh)

Michael Hampsey (2004)
Robert Wood Johnson Medical School-UMDNJ

Lawrence Harshman (2005)
University of Nebraska

R. Scott Hawley (2003)
University of California, Davis

Jotun Hein (2003)
University of Aarhus

Steven Henikoff (2005)
Fred Hutchinson Cancer Center

Nancy A. Jenkins (2004)
National Cancer Institute-FCRDC

Mark Johnston (2003)
Washington University School of Medicine

Thomas C. Kaufman (2003)
Indiana University

David Kingsley (2003)
Stanford University School of Medicine

Christine Kozak (2005)
National Institute of Health-NIAID

Michael Lichten (2003)
National Cancer Institute

A. Javier Lopez (2005)
Carnegie Mellon University

Jennifer J. Loros (2004)
Dartmouth Medical School

Susan Lovett (2004)
Brandeis University

Susan R. McCouch (2005)
Cornell University

Barbara J. Meyer (2005)
University of California, Berkeley

Aaron P. Mitchell (2004)
Columbia University

Alain Nicolas (2003)
Institut Curie

Mohamed Noor (2003)
Louisiana State University

Howard Ochman (2005)
University of Arizona

Peter J. Oefner (2005)
Stanford University

Sara P. Otto (2004)
University of British Columbia

Andrew Paterson (2004)
University of Georgia

Lorraine Pillus (2003)
University of California, San Diego

Patricia J. Pukkila (2004)
University of North Carolina

Mark D. Rose (2004)
Princeton University

Paul Russell (2005)
The Scripps Research Institute

Matthew S. Sachs (2004)
Oregon Health and Science University

Suzanne Sandmeyer (2004)
University of California, Irvine

Outi Savolainen (2005)
University of Oulu

Stephen W. Schaeffer (2003)
The Pennsylvania State University

Trudi Schüpbach (2005)
Princeton University

Michael J. Simmons (2003)
University of Minnesota

Gerald R. Smith (2004)
Fred Hutchinson Cancer Center

Abraham L. Sonenshein (2004)
Tufts University School of Medicine

Tim Stearns (2004)
Stanford University

Wolfgang Stephan (2003)
University of Munich

Venkatesan Sundaresan (2003)
Institute of Molecular Agrobiology

Lorraine S. Symington (2005)
Columbia University College of Physicians and Surgeons

Naoyuki Takahata (2005)
Graduate University, Kanagawa

Simon Tavaré (2005)
University of Southern California

Marcy K. Uyenoyama (2004)
Duke University

Michel A. Veuille (2003)
Ecole Pratique des Hautes Etudes, Paris

Daniel F. Voytas (2005)
Iowa State University

J. Bruce Walsh (2005)
University of Arizona

Detlef Weigel (2005)
Max Planck Institute

Fred Winston (2003)
Harvard Medical School

Zhheng Yang (2005)
University College London

Shozo Yokoyama (2005)
Syracuse University

Miriam E. Zolan (2004)
Indiana University

Managing Editor, Tracey DePellegrin Connelly
Published at Baltimore, Maryland
by the Genetics Society of America

Pre-publication services and printing by Capital City Press, Inc.

VOLUME CONTENTS

to Volume 164, May–August, 2003

Achaz, Guillaume, Eric Coissac, Pierre Netter and Eduardo P. C. Rocha, Associations between inverted repeats and the structural evolution of bacterial genomes 1279–1289

Akashi, Hiroshi, Translational selection and yeast proteome evolution 1291–1303

Albrecht, Kenneth H., Maureen Young, Linda L. Washburn and Eva M. Eicher, *Sry* expression level and protein isoform differences play a role in abnormal testis development in C57BL/6J mice carrying certain *Sry* alleles 277–288

Alonso-Blanco, Carlos, Léonie Bentsink, Corrie J. Hanhart, Hetty Blankestijn-de Vries and Maarten Koornneef, Analysis of natural allelic variation at seed dormancy loci of *Arabidopsis thaliana* 711–729

Anisimova, Maria, Rasmus Nielsen and Ziheng Yang, Effect of recombination on the accuracy of the likelihood method for detecting positive selection at amino acid sites 1229–1236

Augusto-Pinto, Luiz, Santuza M. R. Teixeira, Sérgio D. J. Pena and Carlos Renato Machado, Single-nucleotide polymorphisms of the *Trypanosoma cruzi MSH2* gene support the existence of three phylogenetic lineages presenting differences in mismatch-repair efficiency 117–126

Bachtrog, Doris, and Brian Charlesworth, On the genomic location of the *exuperantia1* gene in *Drosophila miranda*: The limits of *in situ* hybridization experiments 1237–1240

Balakirev, Evgeniy S., V. R. Chechetkin, V. V. Lobzin and Francisco J. Ayala, DNA polymorphism in the β-*esterase* gene cluster of *Drosophila melanogaster* 533–544

Balloux, François, Laurent Lehmann and Thierry de Meeûs, The population genetics of clonal and partially clonal diploids 1635–1644

Barlow, Miriam, and Barry G. Hall, Experimental prediction of the evolution of cefepime resistance from the CMY-2 AmpC β-lactamase 23–29

Beaumont, Mark A., Estimation of population growth or decline in genetically monitored populations 1139–1160

Bennett, Daimark, Balázs Szõor, Sascha Gross, Natalia Vereshchagina and Luke Alphey, Ectopic expression of inhibitors of protein phosphatase type 1 (PP1) can be used to analyze roles of PP1 in Drosophila development 235–245

Betrán, Esther, and Manyuan Long, *Dntf-2r*, a young Drosophila retroposed gene with specific male expression under positive Darwinian selection 977–988

Bhat, Ashwin, Felicite K. Noubissi, Meenal Vyas and Durgadas P. Kasbekar, Genetic analysis of wild-isolated *Neurospora crassa* strains identified as dominant suppressors of repeat-induced point mutation 947–961

Birchler, James A., R. Kelly Dawe and John F. Doebley, Marcus Rhoades, preferential segregation and meiotic drive 835–841

Boase, Natasha A., Robin A. Lockington, Julian R. J. Adams, Louise Rodbourn and Joan M. Kelly, Molecular characterization and analysis of the *acrB* gene of *Aspergillus nidulans*: A gene identified by genetic interaction as a component of the regulatory network that includes the CreB deubiquitination enzyme 95–104

Boivin, Antoine, Christelle Gally, Sophie Netter, Dominique Anxolabéhère and Stéphane Ronsseray, Telomeric associated sequences of Drosophila recruit polycomb-group proteins *in vivo* and can induce pairing-sensitive repression 195–208

Bordenstein, Seth R., Julieanne J. Uy and John H. Werren, Host genotype determines cytoplasmic incompatibility type in the haplodiploid genus Nasonia 223–233

Bowers, Amber K., Jennifer A. Keller and Susan K. Dutcher, Molecular markers for rapidly identifying candidate genes in *Chlamydomonas reinhardtii*: *ERY1* and *ERY2* encode chloroplast ribosomal proteins 1345–1353

Brooks, I. M., R. Felling, F. Kawasaki and R. W. Ordway, Genetic analysis of a synaptic calcium channel in Drosophila: Intragenic modifiers of a temperature-sensitive paralytic mutant of *cacophony* 163–171

Brown, Garth R., Daniel L. Bassoni, Geoffrey P. Gill, Joseph R. Fontana, Nicholas C. Wheeler, Robert A. Megraw, Mark F. Davis, Mitchell M. Sewell, Gerald A. Tuskan and David B. Neale, Identification of quantitative trait loci influencing wood property traits in lob-lolly pine (*Pinus taeda* L.). III. QTL verification and candidate gene mapping 1537–1546

Browning, Sharon, Pedigree data analysis with crossover interference 1561–1566

Bruggeman, Judith, Alfons J. M. Debets, Pieter J. Wijngaarden, J. Arjan G. M. de Visser and Rolf F. Hoekstra, Sex slows down the accumulation of deleterious mutations in the homothallic fungus *Aspergillus nidulans* 479–485

Brunner, S., B. Keller and C. Feuillet, A large rearrangement involving genes and low-copy DNA interrupts the microcollinearity between rice and barley at the *Rph7* locus 673–683

Carney, Ginger E., and Barbara J. Taylor, *logjam* encodes a predicted EMP24/GP25 protein that is required for Drosophila oviposition behavior 173–186

Ch'ng, QueeLim, Lisa Williams, Yung S. Lie, Mary Sym, Jennifer Whangbo and Cynthia Kenyon, Identification of genes that regulate a left-right asymmetric neuronal migration in *Caenorhabditis elegans* 1355–1367

Charlesworth, Deborah, Barbara K. Mable, Mikkel H. Schierup, Carolina Bartolomé and Philip Awadalla, Diversity and linkage of genes in the self-incompatibility gene family in *Arabidopsis lyrata* 1519–1535

Cheng, Rong, Jennie Z. Ma, Fred A. Wright, Shili Lin, Xin Gao, Daolong Wang, Robert C. Elston and Ming D. Li, Nonparametric disequilibrium mapping of functional sites using haplotypes of multiple tightly linked single-nucleotide polymorphism markers 1175–1187

Cheng, Ya-Ming, and Bor-Yaw Lin, Cloning and characterization of maize B chromosome sequences derived from microdissection 299–310

Cheng, Zhi-Jun, and Minoru Murata, A centromeric tandem repeat family originating from a part of Ty3/*gypsy*-retroelement in wheat and its relatives 665–672

Cherry, Joshua L., Selection in a subdivided population with local extinction and recolonization 789–795

Crow, James F., C. C. Tan: A life of peaks and valleys 1–4

de los Santos, Teresa, Neil Hunter, Cindy Lee, Brittany Larkin, Josef Loidl and Nancy M. Hollingsworth, The Mus81/Mms4 endonuclease acts independently of double-Holliday junction resolution to promote a distinct subset of crossovers during meiosis in budding yeast 81–94

Desai, Chand, and Joy Purdy, The neural receptor protein tyrosine phosphatase DPTP69D is required during periods of axon outgrowth in Drosophila 575–588

Desset, Sophie, Carine Meignin, Bernard Dastugue and Chantal Vaury, COM, a heterochromatic locus governing the control of independent endogenous retroviruses from *Drosophila melanogaster* 501–509

Dolgin, Elie S., and Sarah P. Otto, Segregation and the evolution of sex under overdominant selection 1119–1128

Evans, G. J., E. Giuffra, A. Sanchez, S. Kerje, G. Davalos, O. Vidal, S. Illán, J. L. Noguera, L. Varona, I. Velander, O. I. Southwood, D.-J. de Koning, C. S. Haley, G. S. Plastow and L. Anderson, Identification of quantitative trait loci for production traits in commercial pig populations 621–627

Fagundes, Marcia R. Z. Kress, Larissá Fernandes, Marcela Savoldi, Steven D. Harris, Maria H. S. Goldman and Gustavo H. Goldman, Identification of a topoisomerase I mutant, *scsA1*, as an extragenic suppressor of a mutation in *scaA*^{NBS1}, the apparent homolog of human nibrin in *Aspergillus nidulans* 935–945

Falush, Daniel, Matthew Stephens and Jonathan K. Pritchard, Inference of population structure using multilocus genotype data: Linked loci and correlated allele frequencies 1567–1587

Faris, Justin D., John P. Fellers, Steven A. Brooks and Bikram S. Gill, A bacterial artificial chromosome contig spanning the major domestication locus *Q* in wheat and identification of a candidate gene 311–321

Fischer, Sylvia E. J., Erno Wienholds and Ronald H. A. Plasterk, Continuous exchange of sequence information between dispersed Tc1 transposons in the *Caenorhabditis elegans* genome 127–134

Fu, Yun-Xin, and Haying Huai, Estimating mutation rate: How to count mutations? 797–805

Galli, Alvaro, Tiziana Cervelli and Robert H. Schiestl, Characterization of the hyper-recombination phenotype of the *pol3-t* mutation of *Saccharomyces cerevisiae* 65–79

Ganguly, Indrani, Trudy F. C. Mackay and Robert R. H. Anholt, *Scribble* is essential for olfactory behavior in *Drosophila melanogaster* 1447–1457

García-Dorado, Aurora, and Araceli Gallego, Comparing analysis methods for mutation-accumulation data: A simulation study 807–819

Graw, Jochen, Walter Pretsch and Jana Löster, Mutation in intron 6 of the hamster *Mitf* gene leads to skipping of the subsequent exon and creates a novel animal model for the human Waardenburg syndrome type II 1035–1041

Greene, Elizabeth A., Christine A. Codomo, Nicholas E. Taylor, Jorja G. Henikoff, Bradley J. Till, Steven H. Reynolds, Linda C. Enns, Chris Burtner, Jessica E. Johnson, Anthony R. Odden, Luca Comai and Steven Henikoff, Spectrum of chemically induced mutations from a large-scale reverse-genetic screen in Arabidopsis 731–740

Griffith, Jacqulyn L., Laura E. Coleman, Adam S. Raymond, Summer G. Goodson, William S. Pittard, Circe Tsui and Scott E. Devine, Functional genomics reveals relationships between the retrovirus-like Ty1 element and its host *Saccharomyces cerevisiae* 867–879

Hammer, Michael F., Felisa Blackmer, Dan Garrigan, Michael W. Nachman and Jason A. Wilder, Human population structure and its effects on sampling Y chromosome sequence variation 1495–1509

Hanlon, Sean E., David N. Norris and Andrew K. Vershon, Depletion of H2A-H2B dimers in *Saccharomyces cerevisiae* triggers meiotic arrest by reducing *IME1* expression and activating the *BUB2*-dependent branch of the spindle checkpoint 1333–1344

Hernández-Sánchez, Jules, Peter Visscher, Graham Plastow and Chris Haley, Candidate gene analysis for quantitative traits using the transmission disequilibrium test: The example of the melanocortin 4-receptor in pigs 637–644

Hiatt, Evelyn N., and R. Kelly Dawe, Four loci on abnormal chromosome 10 contribute to meiotic drive in maize 699–709

Hsu, F. C., C. J. Wang, C. M. Chen, H. Y. Hu and C. C. Chen, Molecular characterization of a family of tandemly repeated DNA sequences, TR-1, in heterochromatic knobs of maize and its relatives 1087–1097

Huang, Li, Steven A. Brooks, Wanlong Li, John P. Fellers, Harold N. Trick and Bikram S. Gill, Map-based cloning of leaf rust resistance gene *Lr21* from the large and polyploid genome of bread wheat 655–664

James, Avis C., and J. William O. Ballard, Mitochondrial genotype affects fitness in *Drosophila simulans* 187–194

Jenczewski, Eric, Frédérique Eber, Agnès Grimaud, Sylvie Huet, Marie Odile Lucas, Hervé Monod and Anne Marie Chèvre, *PrBn*, a major gene controlling homeologous pairing in oil-seed rape (*Brassica napus*) haploids 645–653

Jiggins, Francis M., Male-killing Wolbachia and mitochondrial DNA: Selective sweeps, hybrid introgression and parasite population dynamics 5–12

Kado, Tomoyuki, Hiroshi Yoshimaru, Yoshihiko Tsumura and Hidenori Tachida, DNA variation in a conifer, *Cryptomeria japonica* (Cupressaceae sensu lato) 1547–1559

Kass, Lee B., Records and recollections: A new look at Barbara McClintock, Nobel-Prize-winning geneticist 1251–1260

Keane, John, and Leon Avery, Mechanosensory inputs influence *Caenorhabditis elegans* pharyngeal activity via ivermectin sensitivity genes 153–162

Kelley, Richard L., and Mitzi I. Kuroda, The Drosophila *roX1* RNA gene can overcome silent chromatin by recruiting the male-specific lethal dosage compensation complex 565–574

Kelly, John K., Deleterious mutations and the genetic variance of male fitness components in *Mimulus guttatus* 1071–1085

Kentner, Edward K., Michael L. Arnold and Susan R. Wessler, Characterization of high-copy-number retrotransposons from the large genomes of the Louisiana iris species and their use as molecular markers 685–697

Kim, Yuseob, and Wolfgang Stephan, Selective sweeps in the presence of interference among partially linked loci 389–398

Knudsen, Bjarne, Michael M. Miyamoto, Philip J. Laipis and David N. Silverman, Using evolutionary rates to investigate protein functional divergence and conservation: A case study of the carbonic anhydrases 1261–1269

Kohn, Michael H., Hans-Joachim Pelz and Robert K. Wayne, Locus-specific genetic differentiation at *Rw* among warfarin-resistant rat (*Rattus norvegicus*) populations 1055–1070

Lafourcade, Céline, Jean-Marc Galan and Matthias Peter, Opposite roles of the F-box protein Rcy1p and the GTPase-activating protein Gyp2p during recycling of internalized proteins in yeast 469–477

Lan, Hong, Jonathan P. Stoehr, Samuel T. Nadler, Kathryn L. Schueler, Brian S. Yandell and Alan D. Attie, Dimension reduction for mapping mRNA abundance as quantitative traits 1607–1614

Laurençon, Anne, Amanda Purdy, Jeff Sekelsky, R. Scott Hawley and Tin Tin Su, Phenotypic analysis of separation-of-function alleles of MEI-41, Drosophila ATM/ATR 589–601

Laval, Guillaume, Magali SanCristobal and Claude Chevalet, Maximum-likelihood and Markov chain Monte Carlo approaches to estimate inbreeding and effective size from allele frequency changes 1189–1204

Law, B., J. S. Buckleton, C. M. Triggs and B. S. Weir, Effects of population structure and admixture on exact tests for association between loci 381–387

Le Corre, Valérie, and Antoine Kremer, Genetic variability at neutral markers, quantitative trait loci and trait in a subdivided population under selection 1205–1219

Lee, Dong W., Robert J. Pratt, Malcolm McLaughlin and Rodolfo Aramayo, An argonaute-like protein is required for meiotic silencing 821–828

Lewis, E. B., C. B. Bridges' repeat hypothesis and the nature of the gene 427–431

Li, Haipeng, Shi-Jie Meng, Zheng-Ming Men, Yun-Xin Fu and Ya-Ping Zhang, Genetic diversity and population history of golden monkeys (*Rhinopithecus roxellana*) 269–275

Li, Jinghong, and Willis X. Li, Drosophila gain-of-function mutant RTK torso triggers ectopic Dpp and STAT signaling 247–258

López-Fanjul, Carlos, Almudena Fernández and Miguel A. Toro, The effect of neutral nonadditive gene action on the quantitative index of population divergence 1627–1633

Lowell, Joanna E., Alexander I. Roughton, Victoria Lundblad and Lorraine Pillus, Telomerase-independent proliferation is influenced by cell type in *Saccharomyces cerevisiae* 909–921

Lukens, Lewis, Fei Zou, Derek Lydiate, Isobel Parkin and Tom Osborn, Comparison of a *Brassica oleracea* genetic map with the genome of *Arabidopsis thaliana* 359–372

Lystig, Theodore C., Adjusted *P* values for genome-wide scans 1683–1687

Malmanche, Nicolas, and Denise V. Clark, Identification of *trans*-dominant modifiers of *Prat* expression in *Drosophila melanogaster* 1419–1433

Mankidy, Rishikesh, Jeremy Hastings and Justin R. Thackeray, Distinct phospholipase C-γ-dependent signaling pathways in the Drosophila eye and wing are revealed by a new *small wing* allele 553–563

Manning, Charlene M., Wendy R. Mathews, Leah P. Fico and Justin R. Thackeray, Phospho-lipase C-γ contains introns shared by src homology 2 domains in unrelated proteins 433–442

Marti, Thomas M., Christophe Kunz and Oliver Fleck, Repair of damaged and mismatched DNA by the XPC homologues Rhp41 and Rhp42 of fission yeast 457–467

Marwan, Wolfgang, Theory of time-resolved somatic complementation and its use to explore the sporulation control network in *Physarum polycephalum* 105–115

Morey, Natalie J., Paul W. Doetsch and Sue Jinks-Robertson, Delineating the requirements for spontaneous DNA damage resistance pathways in genome maintenance and viability in *Saccharomyces cerevisiae* 443–455

Moriyama, Y., and S. Kawano, Rapid, selective digestion of mitochondrial DNA in accordance with the *matA* hierarchy of multiallelic mating types in the mitochondrial inheritance of *Physarum polycephalum* 963–975

Morris, Jason Z., Caryn Navarro and Ruth Lehmann, Identification and analysis of mutations in *bob, Doa* and eight new genes required for oocyte specification and development in *Drosophila melanogaster* 1435–1446

Nagamine, Yoshitaka, Chris S. Haley, Asheber Sewalem and Peter M. Visscher, Quantitative trait loci variation for growth and obesity between and within lines of pigs (*Sus scrofa*) 629–635

Nongthomba, Upendra, Mark Cummins, Samantha Clark, Jim O. Vigoreaux and John C. Sparrow, Suppression of muscle hypercontraction by mutations in the myosin heavy chain gene of *Drosophila melanogaster* 209–222

Nowrousian, Minou, Giles E. Duffield, Jennifer J. Loros and Jay C. Dunlap, The *frequency* gene is required for temperature-dependent regulation of many clock-controlled genes in *Neurospora crassa* 923–933

Ogata, M., H. Ohtani, T. Igarashi, Y. Hasegawa, Y. Ichikawa and I. Miura, Change of the heterogametic sex from male to female in the frog 613–620

Otto, Sarah P., The advantages of segregation and the evolution of sex 1099–1118

Passamonti, Marco, Jeffrey L. Boore and Valerio Scali, Molecular evolution and recombination in gender-associated mitochondrial DNAs of the Manila clam *Tapes philippinarum* 603–611

Percec, Ivona, Joanne L. Thorvaldsen, Robert M. Plenge, Christopher J. Krapp, Joseph H. Nadeau, Huntington F. Willard and Marisa S. Bartolomei, An *N*-ethyl-*N*-nitrosourea mutagenesis screen for epigenetic mutations in the mouse 1481–1494

Pérez-Enciso, Miguel, Miguel A. Toro, Michel Tenenhaus and Daniel Gianola, Combining gene expression and molecular marker information for mapping complex trait genes: A simulation study 1597–1606

Preuss, S. B., and A. B. Britt, A DNA-damage-induced cell cycle checkpoint in Arabidopsis 323–334

Przeworski, Molly, Estimating the time since the fixation of a beneficial allele 1667–1676

Raisin, Sophie, Sophie Pantalacci, Jean-Philippe Brettmayer and Pierre Léopold, A new genetic locus controlling growth and proliferation in *Drosophila melanogaster* 1015–1025

Rannala, Bruce, and Ziheng Yang, Bayes estimation of species divergence times and ancestral population sizes using DNA sequences from multiple loci 1645–1656

Reynolds, K. Tracy, Linda J. Thomson and Ary A. Hoffmann, The effects of host age, host nuclear background and temperature on phenotypic effects of the virulent Wolbachia strain *popcorn* in *Drosophila melanogaster* 1027–1034

Richman, Adam D., L. Gerardo Herrera and Deanna Nash, Evolution of MHC class II Eβ diversity within the genus Peromyscus 289–297

Robin, Stéphanie, Séverine Chambeyron, Alain Bucheton and Isabelle Busseau, Gene silencing triggered by non-LTR retrotransposons in the female germline of *Drosophila melanogaster* 521–531

Ronin, Y., A. Korol, M. Shtemberg, E. Nevo and M. Soller, High-resolution mapping of quantitative trait loci by selective recombinant genotyping 1657–1666

Rosenberg, Noah A., and Aaron E. Hirsh, On the use of star-shaped genealogies in inference of coalescence times 1677–1682

Sabatti, Chiara, Susan Service and Nelson Freimer, False discovery rate in linkage and association genome screens for complex disorders 829–833

Sánchez, Leopoldo, Piter Bijma and John A. Woolliams, Minimizing inbreeding by managing genetic contributions across generations 1589–1595

Satoh, Namiko, Jun-Ichi Itoh and Yasuo Nagato, The *SHOOTLESS2* and *SHOOTLESS1* genes are involved in both initiation and maintenance of the shoot apical meristem through regulating the number of indeterminate cells 335–346

Schlenke, Todd A., and David J. Begun, Natural selection drives Drosophila immune system evolution 1471–1480

Shinohara, Miki, Kazuko Sakai, Tomoko Ogawa and Akira Shinohara, The mitotic DNA damage checkpoint proteins Rad17 and Rad24 are required for repair of double-strand breaks during meiosis in yeast 855–865

Singer, Thorsten, Stefan Haefner, Michael Hoffmann, Michael Fischer, Julia Ilyina and Wolfgang Hilt, Sit4 phosphatase is functionally linked to the ubiquitin-proteasome system 1305–1321

Spencer, Hamish G., Further properties of Gavrilets' one-locus two-allele model of maternal selection 1689–1692

Stuckenholz, Carsten, Victoria H. Meller and Mitzi I. Kuroda, Functional redundancy within *roX1*, a noncoding RNA involved in dosage compensation in *Drosophila melanogaster* 1003–1014

Sundström, Hannah, Matthew T. Webster and Hans Ellegren, Is the rate of insertion and deletion mutation male biased?: Molecular evolutionary analysis of avian and primate sex chromosome sequences 259–268

Tadros, Wael, Simon A. Houston, Arash Bashirullah, Ramona L. Cooperstock, Jennifer L. Semotok, Bruce H. Reed and Howard D. Lipshitz, Regulation of maternal transcript destabilization during egg activation in Drosophila 989–1001

Tanaka, Mark M., Carl T. Bergstrom and Bruce R. Levin, The evolution of mutator genes in bacterial populations: The roles of environmental change and timing 843–854

Tao, Yun, Sining Chen, Daniel L. Hartl and Cathy C. Laurie, Genetic dissection of hybrid incompatibilities between *Drosophila simulans* and *D. mauritiana*. I. Differential accumulation of hybrid male sterility effects on the *X* and autosomes 1383–1398

Tao, Yun, Zhao-Bang Zeng, Jian Li, Daniel L. Hartl and Cathy C. Laurie, Genetic dissection of hybrid incompatibilities between *Drosophila simulans* and *D. mauritiana*. II. Mapping hybrid male sterility loci on the third chromosome 1399–1418

Thomas, Jeffrey H., Craig J. Ceol, Hillel T. Schwartz and H. Robert Horvitz, New genes that interact with *lin-35 Rb* to negatively regulate the *let-60 ras* pathway in *Caenorhabditis elegans* 135–151

Thompson, Dawn A., and Franklin W. Stahl, Genetic control of recombination partner preference in yeast meiosis: Isolation and characterization of mutants elevated for meiotic unequal sister-chromatid recombination (Corrigendum) 1241

Townsend, Jeffrey P., Kaare M. Nielsen, Daniel S. Fisher and Daniel L. Hartl, Horizontal acquisition of divergent chromosomal DNA in bacteria: Effects of mutator phenotypes 13–21

Townsend, Jeffrey P., Kaare M. Nielsen, Daniel S. Fisher and Danile L. Hartl, Horizontal acquisition of divergent chromosomal DNA in bacteria: Effects of mutator phenotypes (Corrigendum) 1241

Veneti, Zoe, Michael E. Clark, Sofia Zabalou, Timothy L. Karr, Charalambos Savakis and Kostas Bourtzis, Cytoplasmic incompatibility and sperm cyst infection in different Drosophila-Wolbachia associations 545–552

Vieira, Cristina P., Paula A. Coelho and Jorge Vieira, Inferences on the evolutionary history of the *Drosophila americana* polymorphic *X/4* fusion from patterns of polymorphism at the *X*-linked *paralytic* and *elav* genes 1459–1469

Vincent, Kevin, Qiang Wang, Steven Jay, Kathryn Hobbs and Brian C. Rymond, Genetic interactions with *CLF1* identify additional pre-mRNA splicing factors and a link between activators of yeast vesicular transport and splicing 895–907

Wakeley, John, and Sabin Lessard, Theory of the effects of population structure and sampling on patterns of linkage disequilibrium applied to genomic data from humans 1043–1053

Wang, Hongyan, Xie Tang and Mohan K. Balasubramanian, Rho3p regulates cell separation by modulating exocyst function in *Schizosaccharomyces pombe* 1323–1331

Wang, Jinliang, Maximum-likelihood estimation of admixture proportions from genetic data 747–765

Waxman, D., and J. R. Peck, The anomalous effects of biased mutation 1615–1626

Whitlock, Michael C., Fixation probability and time in subdivided populations 767–779

Whittaker, John C., Roger M. Harbord, Nicola Boxall, Ian Mackay, Gary Dawson and Richard M. Sibly, Likelihood-based estimation of microsatellite mutation rates 781–787

Wingreen, Ned S., Jonathan Miller and Edward C. Cox, Scaling of mutational effects in models for pleiotropy 1221–1228

Winkler, Christopher R., Nicole M. Jensen, Mark Cooper, Dean W. Podlich and Oscar S. Smith, On the determination of recombination rates in intermated recombinant inbred populations 741–745

Wiuf, Carsten, and David Posada, A coalescent model of recombination hotspots 407–417

Wyatt, Holly R., Hungjiun Liaw, George R. Green and Arthur J. Lustig, Multiple roles for *Saccharomyces cerevisiae* histone H2A in telomere position effect, Spt phenotypes and double-strand-break repair 47–64

Yan, Guiyun, and David W. Severson, Dynamics of molecular markers linked to the resistance loci in a mosquito-plasmodium system 511–519

Yang, Qiong, Xin Xu and Nan Laird, Power evaluations for family-based tests of association with incomplete parental genotypes 399–406

Yi, Nengjun, Varghese George and David B. Allison, Stochastic search variable selection for identifying multiple quantitative trait loci 1129–1138

Yi, Soojin, Doris Bachtrog and Brian Charlesworth, A survey of chromosomal and nucleotide sequence variation in *Drosophila miranda* 1369–1381

Yoshida, Jumpei, Keiko Umezu and Hisaji Maki, Positive and negative roles of homologous recombination in the maintenance of genome stability in *Saccharomyces cerevisiae* 31–46

Yoshida, Shu-hei, Hiba Al-Amodi, Taro Nakamura, Christopher J. McInerny and Chikashi Shimoda, The *Schizosaccharomyces pombe cdt2*$^{+}$ gene, a target of G1-S phase-specific transcription factor complex DSC1, is required for mitotic and premeiotic DNA replication 881–893

Yu, Ning, Michael I. Jensen-Seaman, Leona Chemnick, Judith R. Kidd, Amos S. Deinard, Oliver Ryder, Kenneth K. Kidd and Wen-Hsiung Li, Low nucleotide diversity in chimpanzees and bonobos 1511–1518

Zhang, Hua, Callista Ransom, Philip Ludwig and Steven van Nocker, Genetic analysis of early flowering mutants in Arabidopsis defines a class of pleiotropic developmental regulator required for expression of the flowering-time switch flowering locus C 347–358

Zheng, Qi, Mathematical issues arising from the directed mutation controversy 373–379

Zinser, Erik R., Dominique Schneider, Michel Blot and Roberto Kolter, Bacterial evolution through the selective loss of beneficial genes: Trade-offs in expression involving two loci 1271–1277

Zou, Guohua, Deyun Pan and Hongyu Zhao, Genotyping error detection through tightly linked markers 1161–1173

Zuber, Sophie, Michael J. Hynes and Alex Andrianopoulos, The G-protein α-subunit GasC plays a major role in germination in the dimorphic fungus *Penicillium marneffei* 487–499